SEQUENCE LISTING

```
<110> Igeneon Krebs-Immuntherapie Forschungs- & Entwickl
<120> Immunogenic Recombinant Antibody
<130> Immunogenic Recombinant AB
<140>
<141>
<160> 5
<170> PatentIn Ver. 2.1
<210> 1
<211> 3973
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:mAB 17-1A
<400> 1
ataggetage etegageeac caccatgeat cagaccagea tgggeateaa gatggaatea 60
cagactetgg tetteatate catactgete tggttatatg gagetgatgg gaacattgta 120
atgacccaat ctcccaaatc catgtccatg tcagtaggag agagggtcac cttgacctgc 180
aaggccagtg agaatgtggt tacttatgtt tcntggtatc aacagaaacc agagcagtct 240
cctaaactgc tgatatatgg ggcatccaac cggtacactg gggtcccnga tcgcttcaca 300
ggcagtggat ctgcaacaga tttcactctg accatcagca gtgtgcaggc tgaagacctt 360
gcagattatc actgtggaca gggttacagc tatccgtaca cgttcggagg ggggaccaag 420
ctggaaataa aacgggctga tgctgcacca actgtatcca tcttcccacc atccagtgag 480
cagttaacat ctggaggtgc ctcagtcgtg tgcttcttga acaacttcta ccccaaagac 540
atcaatgtca agtggaagat tgatggcagt gaacgacaaa atggcgtcct gaacagttgg 600
actgatcagg acagcaaaga cagcacctac agcatgagca gcaccctcac gttgaccaag 660
gacgagtatg aacgacataa cagctatacc tgtgaggcca ctcacaagac atcaacttca 720
cccattgtca agagettcaa caggaatgag tgttagacge gtggateege eeeteteeet 780
ccccccccc taacgttact ggccgaagcc gcttggaata aggccggtgt gcgtttgtct 840
atatgtgatt ttccaccata ttgccgtctt ttggcaatgt gagggcccgg aaacctggcc 900
ctgtcttctt gacgagcatt cctaggggtc tttcccctct cgccaaagga atgcaaggtc 960
tgttgaatgt cgtgaaggaa gcagttcctc tggaagcttc ttgaagacaa acaacgtctg 1020
tagcgaccct ttgcaggcag cggaaccccc cacctggcga caggtgcctc tgcggccaaa 1080
agccacgtgt ataagataca cctgcaaagg cggcacaacc ccagtgccac gttgtgagtt 1140
ggatagttgt ggaaagagtc aaatggctct cctcaagcgt attcaacaag gggctgaagg 1200
atgcccagaa ggtaccccat tgtatgggat ctgatctggg gcctcggtgc acatgcttta 1260
catgtgttta gtcgaggtta aaaaaacgtc taggcccccc gaaccacggg gacgtggttt 1320
tcctttgaaa aacacgatga taatatggcc accaccatgg aatggagcag agtctttatc 1380
tttctcctat cagtaactgc aggtgttcac tcccaggtcc agttgcagca gtctggagct 1440
```

```
gagctggtaa ggcctgggac ttcagtgaag gtgtcctgca aggcttctgg atacgccttc 1500
actaattact tgatagagtg ggtaaagcag aggcctggac agggccttga gtggattggg 1560
gtgattaatc ctggaagtgg tggtactaac tacaatgaga agttcaaggg caaggcaaca 1620
ctgactgcag acaaatcctc cagcactgcc tacatgcagc tcagcagcct gacatctgat 1680
gactetgegg tetatttetg tgeaagagat ggteeetggt ttgettaetg gggeeaaggg 1740
actetggtea etgtetetge agecaaaaca acageceeat eggtetatee aetggeeeet 1800
gtgtgtggag atacaactgg ctcctcggtg actctaggat gcctggtcaa gggttatttc 1860
cctgagccag tgaccttgac ctggaactct ggatccctgt ccagtggtgt gcacaccttc 1920
ccagetgtce tgcagtetga cetetacace etcageaget cagtgaetgt aacetegage 1980
acctggccca gccagtccat cacctgcaat gtggcccacc cggcaagcag caccaaggtg 2040
gacaagaaaa ttgagcccag agggcccaca atcaagccct gtcctccatg caaatgccca 2100
gcacctaacc tcttgggtgg accatccgtc ttcatcttcc ctccaaagat caaggatgta 2160
ctcatgatct ccctgagccc catagtcaca tgtgtggtgg tggatgtgag cgaggatgac 2220
ccagatgtcc agatcagctg gtttgtgaac aacgtggaag tacacacagc tcagacacaa 2280
acccatagag aggattacaa cagtactctc cgggtggtca gtgccctccc catccagcac 2340
caggactgga tgagtggcaa ggagttcaaa tgcaaggtca acaacaaaga cctcccagcg 2400
cccatcgaga gaaccatctc aaaacccaaa gggtcagtaa gagctccaca ggtatatgtc 2460
ttgcctccac cagaagaaga gatgactaag aaacaggtca ctctgacctg catggtcaca 2520
gacttcatge etgaagacat ttaegtggag tggaccaaca aegggaaaac agagetaaac 2580
tacaagaaca ctgaaccagt cctggactct gatggttctt acttcatgta cagcaagctg 2640
agagtggaaa agaagaactg ggtggaaaga aatagctact cctgttcagt ggtccacgag 2700
ggtctgcaca atcaccacac gactaagagc ttctcccgga ctccgggtaa atgagtcgac 2760
acgegtegag catgeateta gggeggeeaa tteegeeeet eteeeteee eeceeetaae 2820
gttactggcc gaagccgctt ggaataaggc cggtgtgcgt ttgtctatat gtgatttcc 2880
accatattgc cgtcttttgg caatgtgagg gcccggaaac ctggccctgt cttcttgacg 2940
agcattccta ggggtctttc ccctctcgcc aaaggaatgc aaggtctgtt gaatgtcgtg. 3000
aaggaagcag ttcctctgga agcttcttga agacaaacaa cgtctgtagc gaccctttgc 3060
aggcagcgga accccccacc tggcgacagg tgcctctgcg gccaaaagcc acgtgtataa 3120
gatacacctg caaaggegge acaaccccag tgccacgttg tgagttggat agttgtggaa 3180
agagtcaaat ggctctcctc aagcgtattc aacaaggggc tgaaggatgc ccagaaggta 3240
ccccattgta tgggatctga tctggggcct cggtgcacat gctttacatg tgtttagtcg 3300
aggttaaaaa aacgtctagg cccccgaac cacggggacg tggttttcct ttgaaaaaca 3360
cgatgataag cttgccacaa cccgggatcc tctagaccac catggttcga ccattgaact 3420
gcatcgtcgc cgtgtcccaa gatatgggga ttggcaagaa cggagaccta ccctggcctc 3480
cgctcaggaa cgagttcaag tacttccaaa gaatgaccac aacctcttca gtggaaggta 3540
aacagaatct ggtgattatg ggtaggaaaa cctggttctc cattcctgag aagaatcgac 3600
ctttaaagga cagaattaat atagttctca gtagagaact caaagaacca ccacgaggag 3660
ctcattttct tgccaaaagt ttggatgatg ccttaagact tattgaacaa ccggaattgg 3720
caagtaaagt agacatggtt tggatagtcg gaggcagttc tgtttaccag gaagccatga 3780
atcaaccagg ccacctcaga ctctttgtga caaggatcat gcaggaattt gaaagtgaca 3840
cgtttttccc agaaattgat ttggggaaat ataaacttct cccagaatac ccaggcgtcc 3900
tctctgaggt ccaggaggaa aaaggcatca agtataagtt tgaagtctac gagaagaaag 3960
actaagcggc cgc
                                                                  3973
```

<210> 2

<211> 465

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB 17-1A

<400> 2

Met Glu Trp Ser Arg Val Phe Ile Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

Pro Gly Thr Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe 35 40 45

Thr Asn Tyr Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu 50 55 60

Glu Trp Ile Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn 65 70 75 80

Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser 85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val

Tyr Phe Cys Ala Arg Asp Gly Pro Trp Phe Ala Tyr Trp Gly Gln Gly
115 120 125

Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Ala Pro Ser Val Tyr 130 135 140

Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu 145 150 155 160

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp 165 170 175

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu 180 185 190

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser 195 200 205

Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser 210 215 220

Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys

3

Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val · 310 Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys

<210> 3

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB 17-1A

<400> 3

Met His Gln Thr Ser Met Gly Ile Lys Met Glu Ser Gln Thr Leu Val 1 5 10 15

Phe Ile Ser Ile Leu Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val 20 25 30

Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly Glu Arg Val 35 40 45

Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp 50 55 60

Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala 65 70 75 80

Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser 85 90 95

Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu 100 105 110

Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly
115 120 125

Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val 130 135 140

Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser 145 150 155 160

Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys
165 170 175

Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp 180 185 190

Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu 195 200 205

Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu 210 215 220

Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg 225 230 235 240

Asn Glu Cys

<210> 4

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB 17-1A

<400> 4

Met His Gln Thr Ser Met Gly Ile Lys Met Glu Ser Gln Thr Leu Val 1 5 10 15

Phe Ile Ser Ile Leu Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val 20 25 . 30

Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly Glu Arg Val 35 40 45

Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp 50 55 60

Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala 65 70 75 80

Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser 85 90 95

Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu 100 105 110

Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly 115 120 125

Gly Gly Thr Lys Leu Glu Ile Arg Arg Ala Asp Ala Ala Pro Thr Val 130 135 140

Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser 145 150 155 160

Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys 165 170 175

Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp
180 185 190

Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu
195 200 205

Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu 210 215 220

Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg 225 230 235 240

Asn Glu Cys

<210> 5

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB 17-1A

<400> 5

Met His Gln Thr Ser Met Gly Ile Arg Met Glu Ser Gln Thr Leu Val 1 5 10 15

Phe Ile Ser Ile Leu Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val 20 25 30

Met Thr Gln Ser Pro Arg Ser Met Ser Met Ser Val Gly Glu Arg Val 35 40 45

Thr Leu Thr Cys Arg Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp 50 55 60

Tyr Gln Gln Arg Pro Glu Gln Ser Pro Arg Leu Leu Ile Tyr Gly Ala 65 70 75 80

Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser 85 90 95

Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu

Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Arg Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg

Asn Glu Cys